REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated December 11, 2001, the period for response to which will expire on March 11, 2002.

In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due reconsideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Claims 1-4, 7, 19, 20, 22, and 30-32 are under consideration in this application. Claims 6, 8, 11, 24, 28-29 are being canceled without prejudice or disclaimer, and claims 1, 7, 19, 20, 22 are being amended, as set forth above and in the attached marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention. New claims 30-32 are being added to recite other embodiments described in the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

35 U.S.C. §101 Rejection

Claims 8, 11 and 24 were rejected under 35 U.S.C. § 101 because these claims were considered to be directed to non-statutory subject matter. As indicated above, the claims have been amended so that the rejection should be obviated. Accordingly, the withdrawal of the outstanding indefiniteness rejection under 35 U.S.C. §101 is in order, and is therefore respectfully solicited.

35 U.S.C. §112 Rejection

Claims 6, 24, 28 and 29 were rejected under 35 U.S.C. § 112, second paragraph, as being indefinite. As indicated above, the claims have been amended so that the rejection should be obviated. Accordingly, the withdrawal of the outstanding indefiniteness rejection under 35 U.S.C. §112 is in order, and is therefore respectfully solicited.

Prior Art Rejection

Claims 1-4, 6-8, 11, 19, 20, 22, 24, 28 and 29 were rejected under 35 U.S.C. § 102(b) as being anticipated by WO 98/06872 to Vijg et al., and under 35 U.S.C. § 102(e) as being anticipated by U.S. Pat. No. 6,007,231 to Vijg et al (hereinafter "Vijg"). The rejection has been carefully considered, but is most respectfully traversed.

The present invention is characterized in a primer design system comprising means for selecting at least one DNA nucleotide sequence from a database including a plurality of different DNA nucleotide sequences of the human genome; means for predicting a plurality of different exons of said selected DNA nucleotide and for storing the predicted exons; and a control unit for controlling the system, said control unit controlling: means for extracting a plurality of partial sequences meeting extraction conditions from the predicted exons, wherein said extraction conditions include a predetermined base length; means for determining positions of said plurality of partial sequences related to each one of said predicted exons and the DNA nucleotide sequence; means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said position determining means; means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and means for automatically collating said plurality of pairs of primers with said predicted exons and the DNA nucleotide sequence. The base length is one of the extraction conditions executed independently from the conditions of GC content and Tm.

GENSCAN, GRILL, or RE (page 18, line 9) may be used for predicting unknown exons. The whole method of the present invention, especially the collating step, is performed "automatically" contrary to the prior art that taught that two or more genetic functions can be "manually" collated with their corresponding pairs of primers. The feature of this invention is using genomic DNAs as templates to carry out PCR with primers for different exons in the DNAs, wherein a plurality of primers are designed for different exons which have been predicted by an exon predicting program. Therefore, the exons are **unknown** prior to the predicting step.

Applicants respectfully contend that Vijg fails to teach or suggest predicting unknown exons to be extracted, PCR amplified, and collated. In contrast, Vijg merely teaches simultaneously amplifying many **known** exons of target sequences in the same reaction.

In the invention, primers are designed for many unknown exons in advance. Therefore, it does not need to repeat analyzing the selected exons on at least one target sequence, and primers are designed on the selected sequence in a high throughput way.

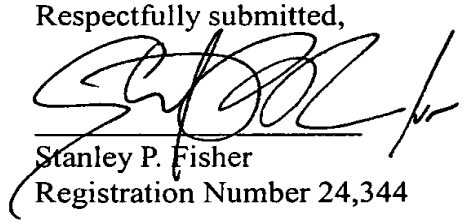
Since Vijg fails to teach or suggest what recited in claim 1, as discussed above, it is respectfully submitted that Vijg does not teach or suggest each and every element of the applicants' invention as now set forth in other independent claims 7, 19, 20, 22 reciting the same novel feature. Accordingly, the withdrawal of the outstanding rejections under 35 U.S.C. §102 is in order, and is respectfully solicited.

In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art references upon which the rejections in the Office Action rely, Applicants respectfully contend that the prior art references cannot anticipate

the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application as amended is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

Respectfully submitted,



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Marked-up Version of Amended Claims

1. A primer design system, comprising:

means for selecting [a plurality of different] at least one DNA nucleotide sequence[s] from a database including a plurality of different DNA nucleotide sequences of the human genome;

means for predicting a plurality of different exons of said selected DNA nucleotide and for storing the predicted exons; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting extraction conditions from the [plurality of different DNA nucleotide sequences] predicted exons, wherein said extraction conditions include a predetermined base length[, the database including exons identified for the DNA nucleotide sequences stored therein];

means for determining positions of said plurality of partial sequences related to each one of said [different] predicted exons and the DNA nucleotide sequence[s, each of said plurality of different partial sequences being extracted from different exons of the same gene];

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said position determining means;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said [different] predicted exons and the DNA nucleotide sequence[s from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted].

7. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of the human genome, said program comprising instructions

for reading data on at least one of the [a] plurality of different DNA nucleotide sequences in said memory,

for predicting a plurality of different exons of said selected DNA nucleotide,

for storing the predicted exons in said memory,

for extracting a plurality of partial sequences meeting extraction conditions from said [plurality of different DNA nucleotide sequences] predicted exons and the data on said [plurality of different] DNA nucleotide sequence[s], wherein said extraction conditions include a predetermined base length[, the data on said plurality of different DNA nucleotide sequences including exons identified for the DNA nucleotide sequences],

for determining positions of said plurality of partial sequences related to each one of said predicted exons and the [different] DNA nucleotide sequence[s, each of said plurality of different partial sequences being extracted from different exons of the same gene],

for selecting a plurality of different partial sequences from results of the determining step, and

for determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences, and

for automatically collating said plurality of pairs of primers with said [different] predicted exons and the DNA nucleotide sequence[s from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted].

19. A primer design system, comprising:

means for selecting [a plurality of different] at least one DNA nucleotide sequence[s] based on at least one predetermined genetic function of interest from a database having data on a plurality of DNA nucleotide sequences of the human genome;

means for predicting and storing a plurality of different exons of said selected DNA nucleotide; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting certain base length extraction conditions from the predicted exons [plurality of different DNA nucleotide sequences, the database including exons identified for the DNA nucleotide sequences stored therein];

means for determining positions of said plurality of partial sequences related to each one of said predicted exons and the [plurality of different] DNA nucleotide sequence[s];

means for selecting a plurality of different partial sequences from said plurality of partial sequences[, each of said plurality of different partial sequences being extracted from different exons of the same gene]; and

means for determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said [different] predicted exons and the DNA nucleotide sequence[s from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted].

20. A primer design system, comprising:

means for selecting [a plurality of different] at least one DNA nucleotide sequence[s] from a database including a plurality of DNA nucleotide sequences of the human genome;

means for predicting and storing a plurality of different exons of said selected DNA nucleotide; and

a control unit for controlling the system, said control unit controlling:

means for associating the predicted exons with corresponding regions in [each of] the [plurality of different] DNA nucleotide sequence[s];

means for extracting a plurality of partial sequences from the predicted exons under extraction conditions, wherein said extraction conditions include a predetermined base length[, the database including exons identified for the DNA nucleotide sequences stored therein];

means for collating positions of said plurality of partial sequences related to each of the predicted exons;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences, wherein more than one partial sequence is associated with a genomic sequence;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with at least the positions related to said [different] predicted exons and the DNA nucleotide sequence[s from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted].

22. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of the human genome, said program comprising instructions

for reading data on [a plurality of different] at least one DNA nucleotide sequence[s] in said memory;

for predicting a plurality of different exons of said selected DNA nucleotide;

for storing the predicted exons in the memory;

for positioning the predicted exons associated with genetic functions of interest on the [plurality of different] DNA nucleotide sequence[s];

for extracting a plurality of partial sequences from the predicted exons under extraction conditions, wherein said extraction conditions include a predetermined base length;

for collating positions of said plurality of partial sequences related to each of the predicted exons and the genetic functions;

for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

for automatically collating said plurality of pairs of primers with at least the positions related to said [different] predicted exons and the DNA nucleotide sequence[s from which said plurality of different partial sequences used to determine said plurality of pairs of primers were extracted].